

Figure 1

5' ... ATAGAATAC A GCATGC TCC CGGCCG CCATGG CCGCGG GATGTC ATG AGG CAA CTA AAC CCT TGC AGC....

SF6 Promoter<| SphI EagI NcoI SacII BspHI

M R Q L N P C S

ANC SEQUENCE....GTC CCC CAA CAA GCT TCA TGC ATA TGG AGT ATG GTC TAG GGATCC

HindIII NdeI BamHI

V P Q Q A S C I W S M V ***

GGGTACC GAGCTC GAATTC GCCCTATA... 3'

KpnI SacI EcoRI |> T7 Promoter

Figure 1

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Figure 2

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1
ATGAGGCAACTAAACCCT**TGC**AGCCAAGAGTTGCAATCACCACAACAATCATATCTGCCG
M R Q L N P **Cys** S Q E L Q S P Q Q S Y L Q

61
CAGCCATATCCACAAAACCCATATCTACCGCAAAAACCATTTCAGTGCAGCAACCGTTT
Q P Y P Q N P Y L P Q K P F P V Q Q P F

121
CACACACCCCAACAATATTTCCCCTATCTACCAGAGGAATTGTTTCCCAATATCAAATA
H T P Q Q Y F P Y L P E E L F P Q Y Q I

181
CCAACCCCCCTACAACCACAACAACCATTCCCCCAACAACCACAACAACCTCTTCCTCGG
P T P L Q P Q Q P F P Q Q P Q Q P L P R

241
CCCCAACAACCATTCCCCTGGCAACCACAACAACCATTTCCCCAGCCCCAAGAACCAATT
P Q Q P F P W Q P Q Q P F P Q P Q E P I

301
CCCCAGCAACCACAACAACCATTCCCACAGCAACCACAACAACCATTCCCACAGCAACCA
P Q Q P Q Q P F P Q Q P Q Q P F P Q Q P

361
CAACAAATAATTTTCAGCAACCCCAACAATCATACCCTGTGCAACCTCAACAGCCATTT
Q Q I I F Q Q P Q Q S Y P V Q P Q Q P F

421 477
CCTCAACAACCTCAACCAGTCCCCCAACAA GCT TCA **TGC**ATATGGAGTATGGTCTAG
P Q Q P Q P V P Q Q A S **Cys** I W S M V ***

Figure 3

HindIII 1 54
AAGCTTCTACCACTCCCACCGCCGTGGCTGTGACTTTCGATCTGACAGCTACCACCACCTAC
A S T T P T A V A V T F D L T A T T T Y

114
GGCGAGAACATCTACCTGGTCGGATCGATCTCTCAGCTGGGTGACTGGGAAACCAGCGAC
G E N I Y L V G S I S Q L G D W E T S D

174
GGCATAGCTCTGAGTGCTGACAAGTACACTTCCAGCGACCCGCTCTGGTATGTCACTGTG
G I A L S A D K Y T S S D P L W Y V T V

234
ACTCTGCCGGCTGGTGAGTCGTTTGAGTACAAGTTTATCCGCATTGAGAGCGATGACTCC
T L P A G E S F E Y K F I R I E S D D S

294
GTGGAGTGGGAGAGTGATCCCAACCGAGAATACACCGTTCCTCAGGCGTGCGGAACGTCG
V E W E S D P N R E Y T V P Q A C G T S

321 NdeI
ACCGCGACGGTGACTGACACCTGGCGGTGCATATGG
T A T V T D T W R C I W

Figure 4

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HindIII

57

AAGCTTTTCGGCAATGAAGATTGCACCCCATGGATGAGTACTCTGATCACTCCACTCCCAAGCA I G N E D C T P W M S T L I T P L P S
CM17. T

117

TGCCGTGACTATGTGGAACAACAAGCATGTGCGCATCGAAACGCCCGGGTCGCCGTACCTC

C R D Y V E Q Q A C R I E T P G S P Y L
. . N . . E M . . P . .

177

GCCAAGCAGCAGTGCTGTGGGGAGCTTGCAAACATTCCGCAGCAGTGCCGATGCCAGGCG

A K Q Q C C G E L A N I P Q Q C R C Q A
. . . E . . E Q

237

CTGCGCTACTTCATGGGGCCGAAGTCTCGTCCGGATCAGAGCGGCCTCATGGAAC TCCCC

L R Y F M G P K S R P D Q S G L M E L P
.

297

GGATGCCCTAGGGAGGTGCAGATGGACTTCGTGAGGATACTCGTCACGCCGGGGTACTGC

G C P R E V Q M D F V R I L V T P G Y C
. N . . P

354

AACTTGACGACCGTTTACAACACTCCGTACTGCCTCGCTATGGAGGAGTCTCAGTGG

N L T T V H N T P Y C L A M E E S Q W
. G

357 NdeI

AGCTGCATATGG

S C I W

Figure 5

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HindIII 57
AAGCTTACGATGTTGCTGGCGGGGGTGGTGCTCAACAATGCCCTGTAGAGACAAAGCTAAAT
A Y D V A G G G G A Q Q C P V E T K L N

117
TCATGCAGGAATTACCTGCTAGATCGATGCTCAACGATGAAGGATTTCCCGGTCACCTGG
S C R N Y L L D R C S T M K D F P V T W

177
CGTTGGTGGAATGGTGGAAGGGAGGTTGTCAAGAGCTCCTTGGGGAGTGTTCAGTCGG
R W W K W W K G G C Q E L L G E C C S R

237
CTCGGCCAAATGCCACCGCAATGCCGCTGCAACATCATCCAGGGGTCAATCCAAGGCGAT
L G Q M P P Q C R C N I I Q G S I Q G D

297
CTCGGTGGCATCTTCGGATTTTCAGCGTGATCGGGCAAGCAAAGTGATACAAGAAGCCAAG
L G G I F G F Q R D R A S K V I Q E A K

300
AACCTGCCGCCCAGGTGCAACCAGGGCCCTCCCTGCAACATCCCCGGCACTATTGGCTAT
N L P P R C N Q G P P C N I P G T I G Y

363 NdeI
TACTGGTGCATATGG
Y W C I W

Figure 6

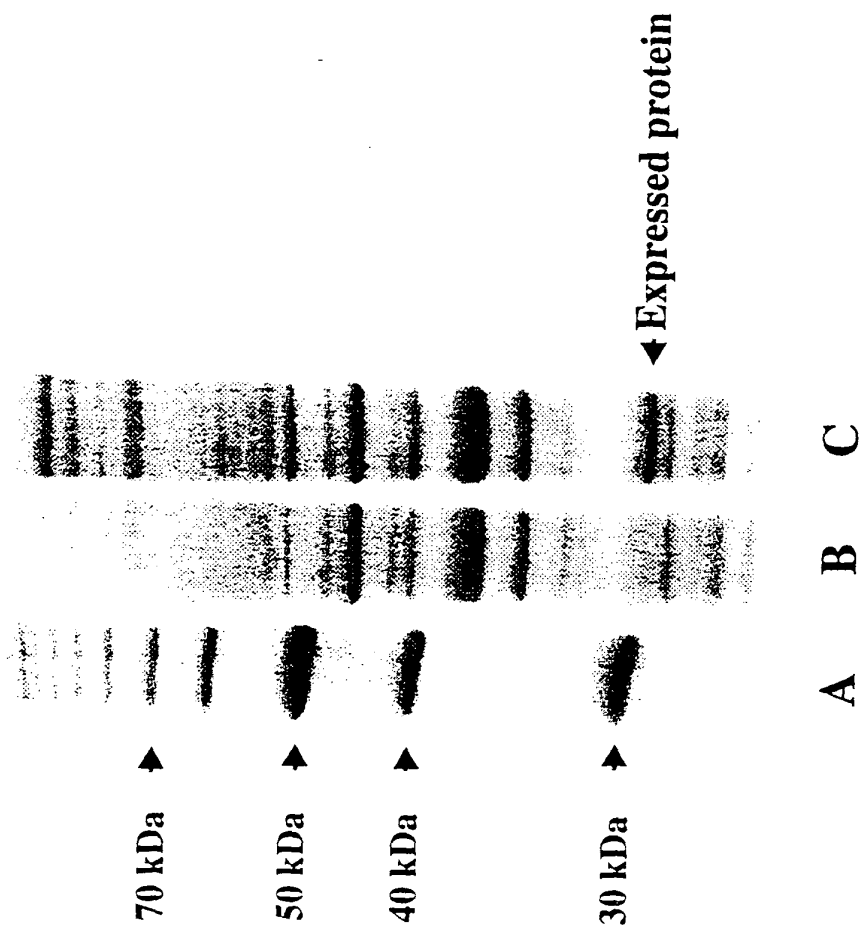


Figure 7

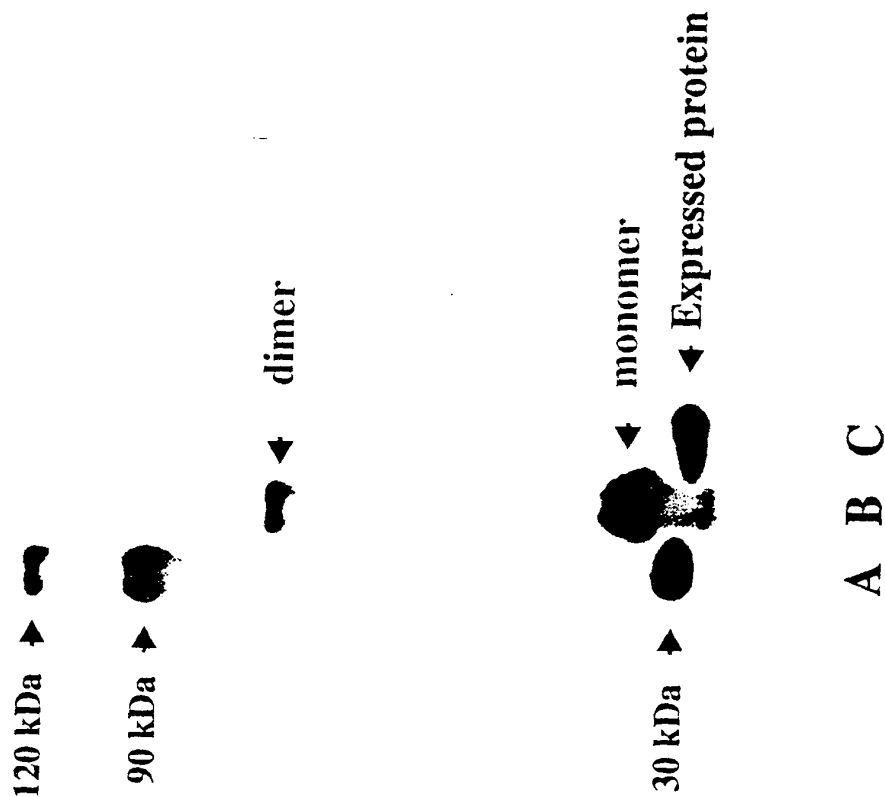


Figure 8

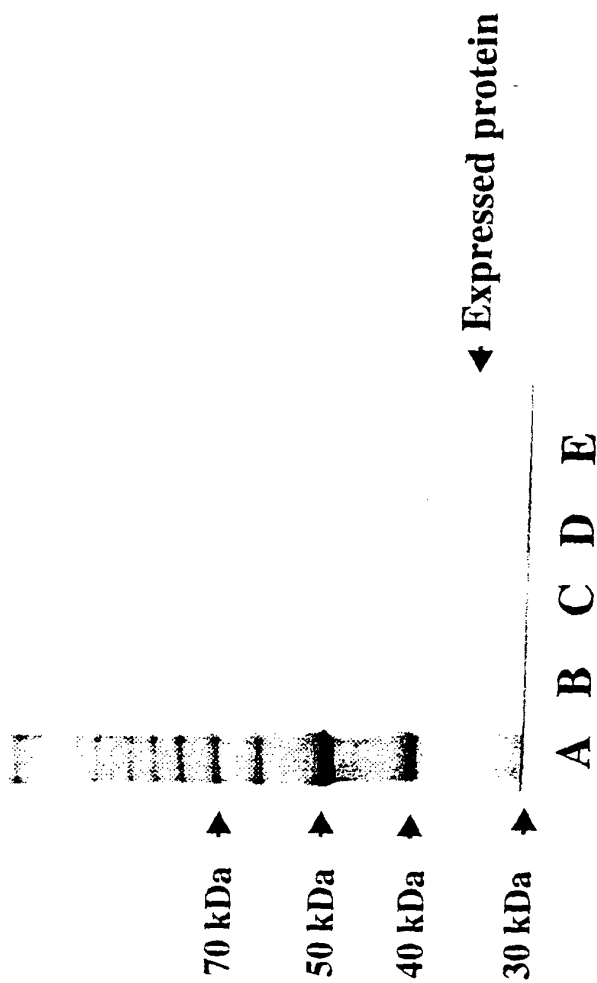


Figure 9

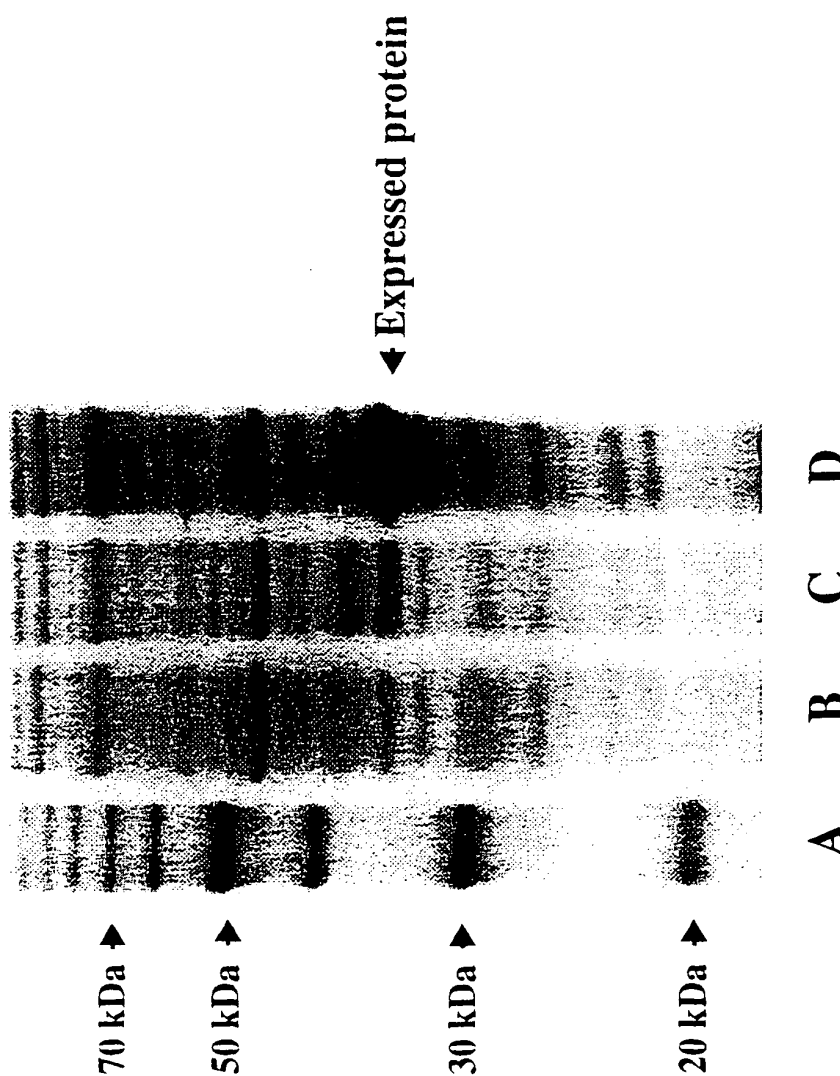


Figure 10

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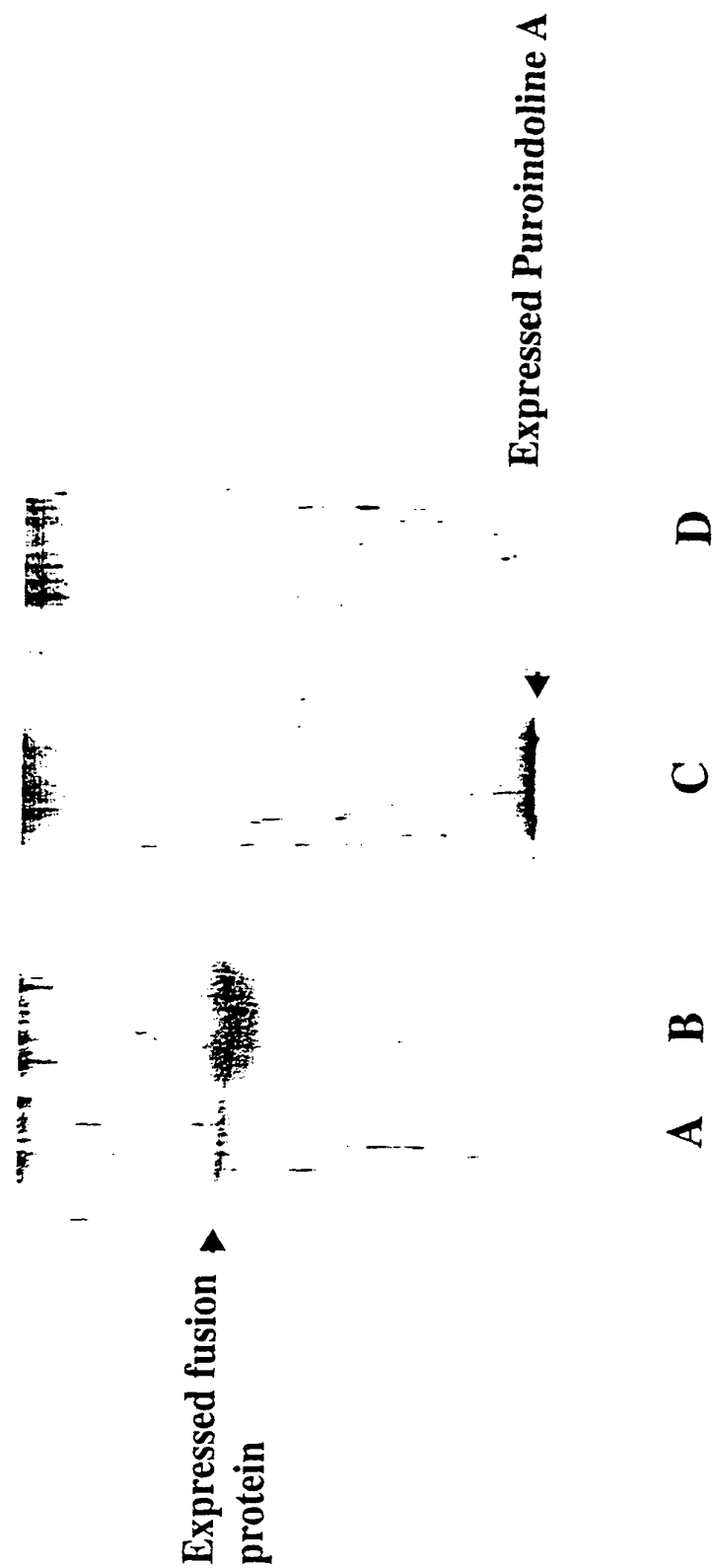


Figure 11

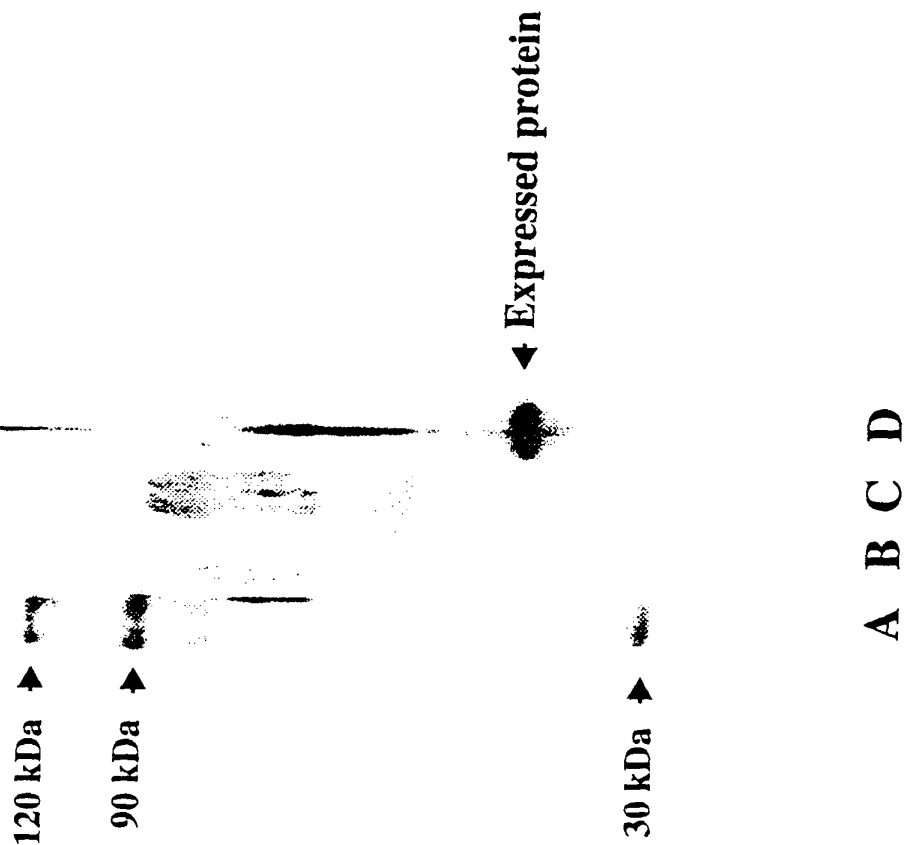


Figure 12

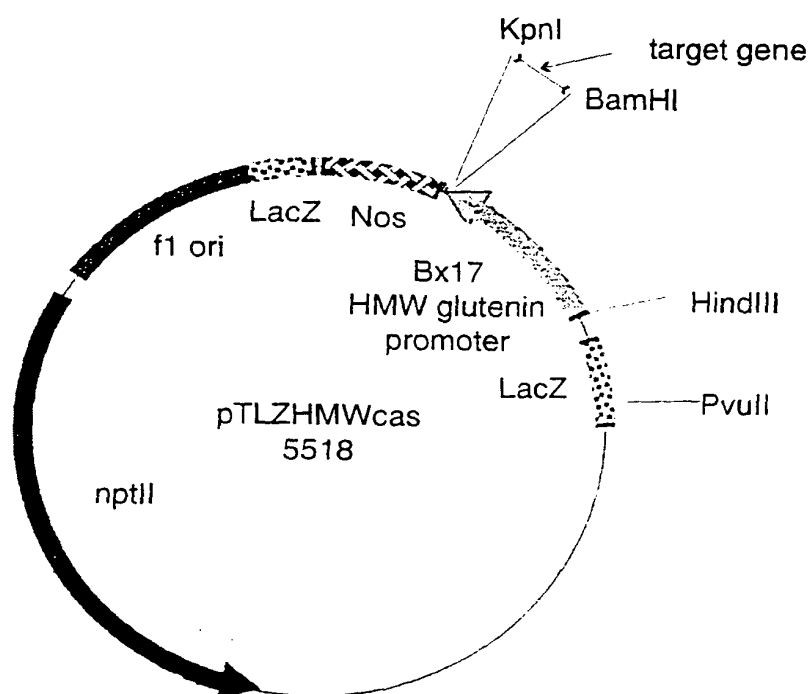


Figure 13

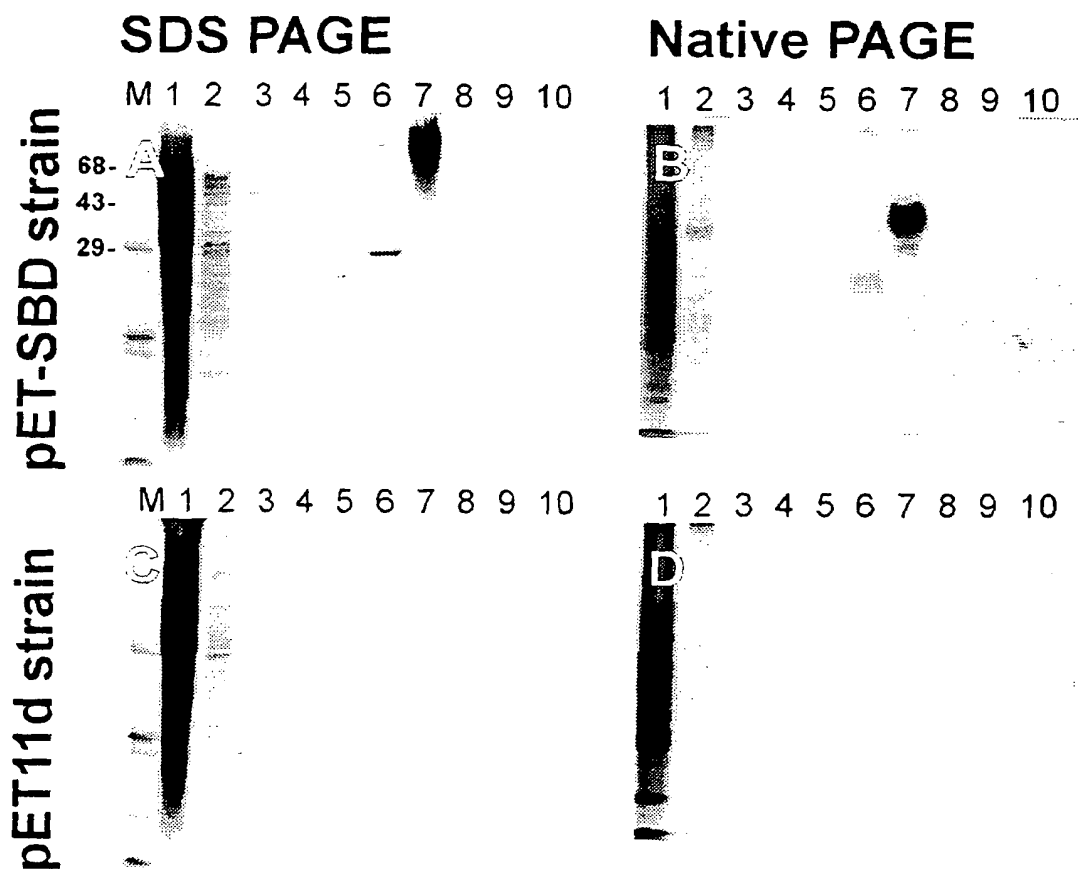


Figure 14

ANGCys7Cys236



binding domain in another protein



ANG/insert/Cys7Cys236



Figure 15

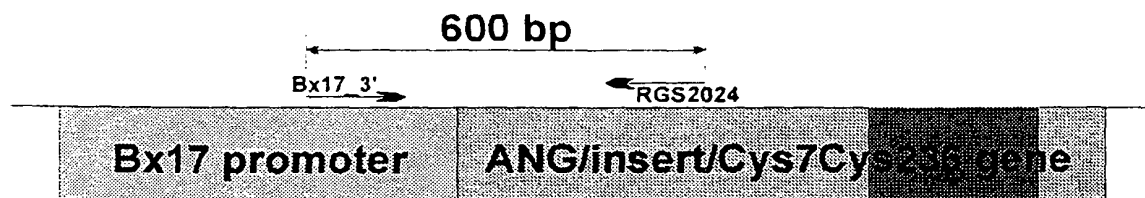


Figure 16

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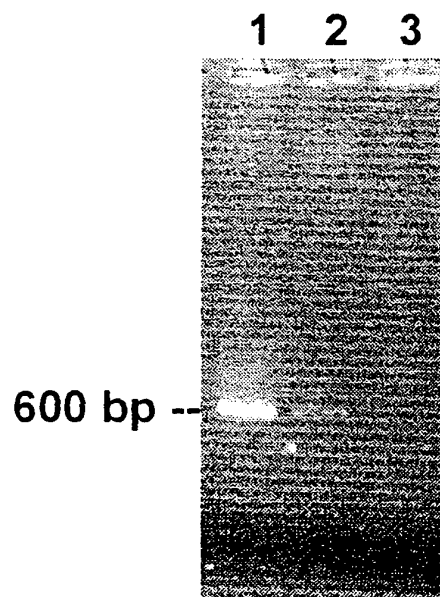


Figure 17

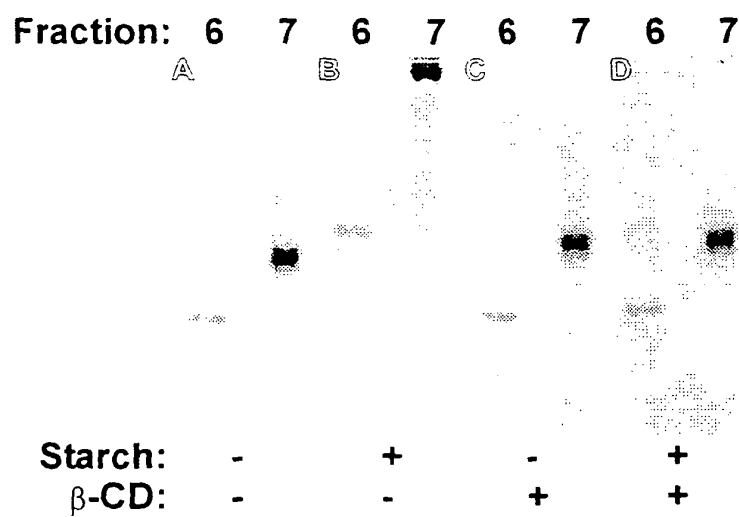


Figure 18

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	M	1	2	3	4	5	6
oxidised		+	+	+	+	-	-
reduced		-	-	+	+	+	+
β -CD		+	-	+	-	+	-

68-

43-

29-

Figure 19